

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: January 24, 2005, 14:36:22 ; Search time 151 Seconds

Perfect score: US-09-744-804A-78
Sequence: 1 MPPRPLILALICGALICAPSLL.....RILPVWAHNRRIALRLELIGC 387

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 202273 seqs, 358723299 residues

Total number of hits satisfying chosen parameters: 444336

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Genesed 23Seq04:*

- 1: genesedGP1990s:*
- 2: genesedGP1990s:*
- 3: genesedGP2000s:*
- 4: genesedGP2001s:*
- 5: genesedGP2002s:*
- 6: genesedGP2003as:*
- 7: genesedGP2003bs:*
- 8: genesedGP2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	54	2.6	9 3	AY82844
2	53	2.5	9 3	AY82840 Lactadherin
3	49	2.3	9 3	AY82841 Lactadherin
4	48	2.3	9 5	ABG32319 HLA-A1/H2
5	46	2.2	9 3	AY82843 Lactadherin
6	45	2.1	9 3	AY82842 Lactadherin
7	45	2.1	10 6	ABG50137
8	45	2.1	10 6	ABG51815
9	45	2.1	10 6	ABG40507
10	45	2.1	10 6	ABG39695
11	45	2.1	10 6	ABG54131
12	45	2.1	10 6	ABG40876
13	45	2.1	10 6	ABG53401
14	45	2.1	10 6	ABG51353
15	45	2.1	10 6	ABG52459
16	45	2.1	10 6	ABG50895
17	44	2.1	9 3	AY82846 Lactadherin
18	44	2.1	10 6	ABG42681
19	44	2.1	9 6	ABG44746
20	44	2.1	9 6	ABG44094
21	44	2.1	9 6	ABG46023
22	44	2.1	9 6	ABG48298
23	44	2.1	9 6	ABG47602
24	44	2.1	9 6	ABG41130
25	44	2.1	9 6	ABG48967

RESULT 1	
AY82844	AY82844 standard; peptide; 9 AA.
XX	
XX	AY82844;
XX	
DT	19-JUN-2000 (first entry)
DB	lactadherin (BA-46) peptide fragment (tumour associated antigen).
XX	
KW	Tumour associated antigen peptide; TAA; cancer; carcinoma; treatment; prevention; cure; anti-tumour vaccine; metastases; breast; bladder; prostate; pancreas; ovary; thyroid; colon; stomach; carcinoma; uroplakin; MHC Class I; HLA-A2; human; Major Histocompatibility Complex; prostate specific antigen; prostate specific membrane antigen; prostate acid phosphatase; mucin; lactadherin; teratocarcinoma derived growth factor; PSA; PSMA; PAP; CRIPTO-1.
XX	
OS	Homo sapiens.
XX	
PN	WO200006723-A1.
XX	
PD	10-FEB-2000.
XX	
PF	29-JUL-1999; 99WO-IL000417.
XX	
PR	30-JUL-1998; 98IL-0012608.
XX	
PA	(YEDA) YEDA RES & DEV CO LTD.
PA	(BIOT-) BIO-TECHNOLOGY GEN CORP.
XX	
PI	Eisenbach L, Carmon L, Tirosh B, Bar-Haim B, Paz A, Fridkin M;
PI	Fitzter-Attas C;
XX	
DR	WPI: 2000-205463/18.
XX	
PT	Tumor associated antigen peptides, especially derived from uroplakin, useful as vaccines to prevent or cure cancers including breast, bladder, prostate, pancreas, ovary, thyroid, colon and stomach.
CC	breast, bladder, prostate, ovaries, thyroid, colon, stomach, head or neck cancer or a carcinoma. The tumor associated antigens are presentable to the immune system by HLA-A2 molecules and are generally between 8 to 10 amino acids in length. The amino acids located at

CC presentable to the immune system by HLA-A2 molecules and are generally
 CC between 8 to 10 amino acids in length. The amino acids located at
 CC positions 2 and 9 of the tumour associated antigens are the anchor
 CC residues which participate in the binding to MHC class I molecules, more
 CC specifically HLA-A2. More tumour associated antigens are described in
 CC GENSEQ records AAY82806-Y82882. Those tumour associated antigens
 CC described in records AAY82806-Y82824 and AAY82855-Y82869 are derived
 CC from Uroplakin, such as Uroplakin II, Uroplakin Ia, Uroplakin III and
 CC Uroplakin Ib. Those described in records AAY82855-Y82829 are derived from
 CC prostate specific antigen (PSA). Those described in records AAY82830-
 CC 82835 are derived from prostate specific membrane antigen (PSMA). Those
 CC described in records YY82836-AAY82839 are derived from prostate acid
 CC phosphatase (PAP). Those described in records AAY82840-Y82845 are derived
 CC from Lactadherin (BA-46). Those described in records AAY82847-Y82854 are
 CC derived from Mucin and those described in records AAY82871-Y82882 are
 CC derived from Teratocarcinoma derived growth factor (CRYPTO-1)

SQ Sequence 9 AA;

QY

Query Match

Best Local Similarity 2.3%; score 49; DB 3; Length 9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

1

NULLRRMMWV 9

QY

Query Match

Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

1

NULLRRMMWV 139

SQ Sequence 9 AA;

QY

Query Match

Best Local Similarity 2.3%; score 49; DB 3; Length 9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

1

NULLRRMMWV 139

SQ Sequence 9 AA;

QY

Query Match

Best Local Similarity 2.3%; score 48; DB 5; Length 9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

1

HEVILKAFKV 160

SQ Sequence 9 AA;

QY

Query Match

Best Local Similarity 2.3%; score 48; DB 5; Length 9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

1

HEVILKAFKV 9

SQ Sequence 9 AA;

QY

Query Match

Best Local Similarity 2.3%; score 48; DB 5; Length 9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

1

HEVILKAFKV 9

SQ Sequence 9 AA;

QY

Query Match

Best Local Similarity 2.3%; score 48; DB 5; Length 9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

1

HEVILKAFKV 9

SQ Sequence 9 AA;

QY

Query Match

Best Local Similarity 2.3%; score 48; DB 5; Length 9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

1

HEVILKAFKV 9

SQ Sequence 9 AA;

QY

Query Match

Best Local Similarity 2.3%; score 48; DB 5; Length 9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

1

HEVILKAFKV 9

SQ Sequence 9 AA;

QY

Query Match

Best Local Similarity 2.3%; score 48; DB 5; Length 9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

1

HEVILKAFKV 9

SQ Sequence 9 AA;

QY

Query Match

Best Local Similarity 2.3%; score 48; DB 5; Length 9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

1

HEVILKAFKV 9

SQ Sequence 9 AA;

QY

Query Match

Best Local Similarity 2.3%; score 48; DB 5; Length 9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

1

HEVILKAFKV 9

SQ Sequence 9 AA;

QY

Query Match

Best Local Similarity 2.3%; score 48; DB 5; Length 9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

1

HEVILKAFKV 9

SQ Sequence 9 AA;

QY

Query Match

Best Local Similarity 2.3%; score 48; DB 5; Length 9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

1

HEVILKAFKV 9

SQ Sequence 9 AA;

QY

Query Match

Best Local Similarity 2.3%; score 48; DB 5; Length 9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

1

HEVILKAFKV 9

SQ Sequence 9 AA;

QY

Query Match

Best Local Similarity 2.3%; score 48; DB 5; Length 9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

1

HEVILKAFKV 9

SQ Sequence 9 AA;

QY

Query Match

Best Local Similarity 2.3%; score 48; DB 5; Length 9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

1

HEVILKAFKV 9

SQ Sequence 9 AA;

QY

Query Match

Best Local Similarity 2.3%; score 48; DB 5; Length 9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

1

HEVILKAFKV 9

SQ Sequence 9 AA;

QY

Query Match

Best Local Similarity 2.3%; score 48; DB 5; Length 9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

1

HEVILKAFKV 9

SQ Sequence 9 AA;

QY

Query Match

Best Local Similarity 2.3%; score 48; DB 5; Length 9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

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HEVILKAFKV 9

SQ Sequence 9 AA;

QY

Query Match

Best Local Similarity 2.3%; score 48; DB 5; Length 9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

1

HEVILKAFKV 9

SQ Sequence 9 AA;

QY

Query Match

Best Local Similarity 2.3%; score 48; DB 5; Length 9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

1

HEVILKAFKV 9

SQ Sequence 9 AA;

QY

Query Match

Best Local Similarity 2.3%; score 48; DB 5; Length 9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

1

HEVILKAFKV 9

SQ Sequence 9 AA;

QY

Query Match

Best Local Similarity 2.3%; score 48; DB 5; Length 9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

1

HEVILKAFKV 9

SQ Sequence 9 AA;

QY

Query Match

Best Local Similarity 2.3%; score 48; DB 5; Length 9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

1

HEVILKAFKV 9

SQ Sequence 9 AA;

QY

Query Match

Best Local Similarity 2.3%; score 48; DB 5; Length 9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

1

HEVILKAFKV 9

SQ Sequence 9 AA;

QY

Query Match

Best Local Similarity 2.3%; score 48; DB 5; Length 9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

1

HEVILKAFKV 9

SQ Sequence 9 AA;

QY

Query Match

Best Local Similarity 2.3%; score 48; DB 5; Length 9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

1

HEVILKAFKV 9

SQ Sequence 9 AA;

QY

Query Match

Best Local Similarity 2.3%; score 48; DB 5; Length 9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

1

HEVILKAFKV 9

SQ Sequence 9 AA;

QY

Query Match

Best Local Similarity 2.3%; score 48; DB 5; Length 9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

1

HEVILKAFKV 9

SQ Sequence 9 AA;

QY

Query Match

Best Local Similarity 2.3%; score 48; DB 5; Length 9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

1

HEVILKAFKV 9

SQ Sequence 9 AA;

QY

Query Match

Best Local Similarity 2.3%; score 48; DB 5; Length 9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

1

HEVILKAFKV 9

SQ Sequence 9 AA;

QY

Query Match

Best Local Similarity 2.3%; score 48; DB 5; Length 9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

1

HEVILKAFKV 9

SQ Sequence 9 AA;

QY

Query Match

Best Local Similarity 2.3%; score 48; DB 5; Length 9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

1

HEVILKAFKV 9

SQ Sequence 9 AA;

QY

Query Match

Best Local Similarity 2.3%; score 48; DB 5; Length 9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

1

HEVILKAFKV 9

SQ Sequence 9 AA;

QY

Query Match

Best Local Similarity 2.3%; score 48; DB 5; Length 9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

1

HEVILKAFKV 9

SQ Sequence 9 AA;

QY

Query Match

Best Local Similarity 2.3%; score 48; DB 5; Length 9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

1

HEVILKAFKV 9

SQ Sequence 9 AA;

QY

Query Match

Best Local Similarity 2.3%; score 48; DB 5; Length 9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

1

HEVILKAFKV 9

SQ Sequence 9 AA;

QY

Query Match

Best Local Similarity 2.3%; score 48; DB 5; Length 9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

1

HEVILKAFKV 9

SQ Sequence 9 AA;

QY

Query Match

Best Local Similarity 2.3%; score 48; DB 5; Length 9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

1

HEVILKAFKV 9

SQ Sequence 9 AA;

QY

Query Match

Best Local Similarity 2.3%; score 48; DB 5; Length 9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

1

HEVILKAFKV 9

SQ Sequence 9 AA;

QY

Query Match

Best Local Similarity 2.3%; score 48; DB 5; Length 9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

1

HEVILKAFKV 9

PS claim 17; Page 100; 113pp; English.

XX

CC Tumour associated antigen peptides (TAA) may be used for the treatment, prevention and cure of cancer or cancer metastases. The cancer may be, breast, bladder, prostate, pancreas, ovary, thyroid, colon, stomach, head or neck cancer or a carcinoma. The tumour associated antigens are presentable to the immune system by HLA-A2 molecules and are generally between 8 to 10 amino acids in length. The amino acids located at positions 2 and 9 of the tumour associated antigens are the anchor residues which participate in the binding to MHC class I molecules, more specifically HLA-A2. More tumour associated antigens are described in GENESSEQ records AAY82806-Y82824. Those tumour associated antigens described in records AAY82806-Y82824 and AAY82855-Y82859 are derived from Uroplakin, such as Uroplakin II, Uroplakin Ia, Uroplakin III and Uroplakin Ib. Those described in records AAY82825-Y82829 are derived from prostate specific antigen (PSA). Those described in records AAY82830-Y82835 are derived from prostate specific membrane antigen (PSMA). Those described in records YY82836-AY82839 are derived from prostate acid phosphatase (PAP). Those described in records AAY82840-Y82845 are derived from Lactadherin (BA-46). Those described in records AAY82847-Y82854 are derived from Mucin and those described in records AAY82871-Y82882 are derived from Teratocarcinoma derived growth factor (CRYPTO-1).

CC

PS claim 17; Page 99; 113pp; English.

XX

CC Tumour associated antigen peptides (TAA) may be used for the treatment, prevention and cure of cancer or cancer metastases. The cancer may be, breast, bladder, prostate, pancreas, ovary, thyroid, colon, stomach, head or neck cancer or a carcinoma. The tumour associated antigens are presentable to the immune system by HLA-A2 molecules and are generally between 8 to 10 amino acids in length. The amino acids located at positions 2 and 9 of the tumour associated antigens are the anchor residues which participate in the binding to MHC class I molecules, more specifically HLA-A2. More tumour associated antigens are described in GENESSEQ records AAY82806-Y82882. Those tumour associated antigens described in records AAY82806-Y82824 and AAY82855-Y82859 are derived from Uroplakin, such as Uroplakin II, Uroplakin Ia, Uroplakin III and Uroplakin Ib. Those described in records AAY82825-Y82829 are derived from prostate specific antigen (PSA). Those described in records AAY82830-Y82835 are derived from prostate specific membrane antigen (PSMA). Those described in records YY82836-AY82839 are derived from prostate acid phosphatase (PAP). Those described in records AAY82840-Y82845 are derived from Lactadherin (BA-46). Those described in records AAY82847-Y82854 are derived from Mucin and those described in records AAY82871-Y82882 are derived from Teratocarcinoma derived growth factor (CRYPTO-1).

CC

PS New 15P3D4 proteins and genes useful for eliciting a humoral or cellular immune response, or for diagnosing, prognosing, preventing or treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer or carcinoma.

PT

CC The invention relates to a novel composition comprising a substance that
 CC modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or
 CC a molecule that is modulated by the 151P3D4 protein, where the status of
 CC a cell that expresses the 151P3D4 protein is modulated. The novel
 CC compositions, or the 151P3D4 proteins and genes, are useful for eliciting
 CC a humoral or cellular immune response. The 151P3D4 genes and proteins
 CC are also useful for diagnosing, prognosis, preventing or treating
 CC cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or
 CC bronchial cancer, breast cancer or carcinoma. This sequence represents a
 CC the invention
 CC sequence 10 AA;

SQ

Query	Match	Best Local Similarity	Score	DB	Length	Matches	Pred	NO.	Mismatches	Indels	Gaps	0
Qy	299	VRGIFTQGAR	308		10	9;	Conservative	9	0;	0	0	0
Db	1	VRGIFTQGAK	10		10	+						

RESULT 8

ABJ51815 2.1%; Score 45; DB 6; length 10;
 ID ABJ51815 standard; peptide; 10 AA.

XX

AC ABJ51815;

XX

DT 16-OCT-2003 (first entry)

XX

DE 151P3D4 cancer gene related HLA peptide #9635.

XX

KW Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoural; cancer;
 cellular immune response; adenocarcinoma; bladder; colorectal; lung;
 bronchial; breast; carcinoma; human leukocyte antigen; HLA.

XX

OS Homo sapiens.

XX

PN WO200283860-A2.

XX

PD 24-OCT-2002.

XX

PP 09-APR-2002; 2002WO-US011644.

XX

PR 10-APR-2001; 2001US-0282739P.

XX

PR 25-APR-2001; 2001US-0286630P.

PA (AGEN-) AGENSY INC.

XX

PT Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison K;

PI Morrison RK, Ge W, Jakobovits A;

XX

DR WPI; 2003-167091/16.

PT New 151P3D4 proteins and genes, useful for eliciting a humoral or
 PT cellular immune response, or for diagnosing, prognosis, preventing or
 PT treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer
 or carcinoma.

XX

PS Claim 13; Page 251; 428pp; English.

XX

CC The invention relates to a novel composition comprising a substance that
 CC modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or
 CC a molecule that is modulated by the 151P3D4 protein, where the status of
 CC a cell that expresses the 151P3D4 protein is modulated. The novel
 CC compositions, or the 151P3D4 proteins and genes, are useful for eliciting
 CC a humoral or cellular immune response. The 151P3D4 genes and proteins
 CC are also useful for diagnosing, prognosis, preventing or treating
 CC cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or
 CC bronchial cancer, breast cancer or carcinoma. This sequence represents a
 CC human leukocyte antigen peptide relating to the 151P3D4 composition of
 CC the invention

CC. Line invention
XX
sq. sequence 10 AA;
Query Match 2.1%; Score 45; DB 6; Length 10;
Best Local Similarity 90.0%; Pred. No. 9.3e+03;
Matches 9; Conservative 1; Mismatches 0; Indels 0;
Gaps 0;
OY 299 VVGIITGCGAR 308
DB |||||: 1 VVGIITGCGAK 10

RESULT 10
 ABJ3995
 ABJ39695 standard; peptide; 10 AA.
 XX
 AC ABJ3995;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE 151P3D4 cancer gene related peptide #322.
 XX
 KW Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoural; cancer;
 KW cellular immune response; adenocarcinoma; bladder; colorectal; lung;
 KW bronchial; breast; carcinoma.
 XX
 OS Unidentified.
 XX
 PN WO200283860-A2.
 XX
 PD 24-OCT-2002.
 DR
 XX
 PF 09-APR-2002; 2002WO-US011644.
 XX
 PR 10-APR-2001; 2001US-0282739P.
 XX
 PR 25-APR-2001; 2001US-0286630P.
 XX
 PA (AGEN-) AGENSYN INC.
 XX
 PT Challita-Eid PM, Raitano AB, Paris M, Hubert RS, Morrison K;
 PT Morrison RK, Ge W, Jakobovits A;
 XX
 WPI; 2003-167091/16.
 XX
 New 151P3D4 proteins and genes, useful for eliciting a humoral or
 PT cellular immune response, or for diagnosing, prognosis, preventing or
 PT treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer
 PT or carcinoma.
 XX
 PA (AGEN-) AGENSYN INC.
 XX
 PT Challita-Eid PM, Raitano AB, Paris M, Hubert RS, Morrison K;
 PT Morrison RK, Ge W, Jakobovits A;
 XX
 WPI; 2003-167091/16.
 XX
 The invention relates to a novel composition comprising a substance that
 CC modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or
 CC a molecule that is modulated by the 151P3D4 protein, where the status of
 CC a cell that expresses the 151P3D4 protein is modulated. The novel
 CC compositions, or the 151P3D4 protein and genes, are useful for eliciting
 CC a humoral or cellular immune response. The 151P3D4 genes and proteins
 CC are also useful for diagnosing, prognosis, preventing or treating
 CC cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or
 CC bronchial cancer, breast cancer or carcinoma. This sequence represents a
 CC human leukocyte antigen peptide relating to the 151P3D4 composition of
 CC the invention
 XX
 SQ Sequence 10 AA;
 Query Match 2.1%; Score 45; DB 6; Length 10;
 Best Local Similarity 90.0%; Pred. No. 9.3e+03;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 299 VIGITQGAR 308
 DB 1 VIGITQGAK 10
 SQ Sequence 10 AA;
 RESULT 12
 ABJ40876
 ID ABJ40876 standard; peptide; 10 AA.
 XX
 AC ABJ40876;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE 151P3D4 cancer gene related peptide #1503.
 XX
 KW Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoural; cancer;
 KW cellular immune response; adenocarcinoma; bladder; colorectal; lung;
 KW bronchial; breast; carcinoma.
 XX
 OS Unidentified.
 XX
 PN WO200283860-A2.
 XX
 PD 24-OCT-2002.
 XX
 PR 09-APR-2002; 2002WO-US011644.
 XX
 PR 09-APR-2002; 2002WO-US011644.

RESULT 11
 ABJ54131
 ABJ54131 standard; peptide; 10 AA.
 ID ABJ54131
 XX
 AC ABJ54131;
 XX
 DT 16-OCT-2003 (first entry)
 XX
 DE 151P3D4 cancer gene related HLA peptide #11951.
 XX
 KW Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoural; cancer;

PR 10-APR-2001; 2001US-0282739P.
 PR 25-APR-2001; 2001US-0286630P.
 XX
 PA (AGEN-) AGENSYN INC.
 XX
 PT Challita-Eid PM, Raitano AB, Paris M, Hubert RS, Morrison K;
 PI Morrison RK, Ge W, Jakobovits A;
 XX DR WPI; 2003-167091/16.
 XX
 PT New 151P3D4 proteins and genes, useful for eliciting a humoral or
 PT cellular immune response, or for diagnosing, prognosis, preventing or
 PT treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer
 XX or carcinoma.
 XX
 PS Claim 13; Page 142; 426pp; English.
 XX
 CC The invention relates to a novel composition comprising a substance that
 CC modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or
 CC a molecule that is modulated by the 151P3D4 protein, where the status of
 CC a cell that expresses the 151P3D4 protein is modulated. The novel
 CC compositions, or the 151P3D4 proteins and genes, are useful for eliciting
 CC a humoral or cellular immune response. The 151P3D4 genes and proteins
 CC are also useful for diagnosing, prognosis, preventing or treating
 CC cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or
 CC bronchial cancer, breast cancer or carcinoma. This sequence represents a
 CC 151P3D4 related peptide of the invention
 XX
 SQ Sequence 10 AA;
 CC
 CC Best Local Similarity 90.0%; Pred. No. 9.3e+03; Mismatches 9; Indels 0; Gaps 0;
 CC Matches 9; Conservative 1;
 CC
 QY 299 VIGIITQGAR 308
 DB 1 VIGIITQGAK 10
 XX
 RESULT 13
 ABJ53401
 ID ABJ53401 Standard; peptide; 10 AA.
 AC ABJ53401;
 XX DT 16-OCT-2003 (first entry)
 DR 151P3D4 cancer gene :related HLA peptide #11221.
 XX
 KW Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoural; cancer;
 KW cellular immune response; adenocarcinoma; bladder; colorectal; lung;
 KW bronchial; breast; carcinoma; human leukocyte antigen; HLA.
 OS Homo sapiens.
 XX PN WO200283860-A2.
 XX PD 24-OCT-2002.
 XX PR 09-APR-2002; 2002WO-US011644.
 XX PR 10-APR-2001; 2001US-0282739P.
 XX PR 25-APR-2001; 2001US-0286630P.
 XX PA (AGEN-) AGENSYN INC.
 XX
 PT Challita-Eid PM, Raitano AB, Paris M, Hubert RS, Morrison K;
 PI Morrison RK, Ge W, Jakobovits A;
 XX DR WPI; 2003-167091/16.
 XX
 PT New 151P3D4 proteins and genes, useful for eliciting a humoral or
 PT cellular immune response, or for diagnosing, prognosis, preventing or
 PT treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer
 XX or carcinoma.
 XX
 PS Claim 13; Page 246; 426pp; English.
 XX
 CC The invention relates to a novel composition comprising a substance that
 CC modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or
 CC a molecule that is modulated by the 151P3D4 protein, where the status of
 CC a cell that expresses the 151P3D4 protein is modulated. The novel
 CC compositions, or the 151P3D4 proteins and genes, are useful for eliciting
 CC a humoral or cellular immune response. The 151P3D4 genes and proteins

CC are also useful for diagnosing, prognosis, preventing or treating
 CC cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or
 CC bronchial cancer, breast cancer or carcinoma. This sequence represents a
 CC human leukocyte antigen peptide relating to the 151P3D4 composition of
 CC the invention

SQ Sequence 10 AA;

QY	299	VIGIITQGAR	308
Db			:
	1	VIGIITQGAK	10

Query Match 2.1%; Score 45; DB 6; Length 10;
 Best Local Similarity 90.0%; Pred. No. 9.3e+03;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 299 VIGIITQGAR 308
 Db 1 VIGIITQGAK 10

RESULT 15

ABJ5249 ABJ52549 standard; peptide; 10 AA.

XX

AC ABJ52549;

XX

DT 15-OCT-2003. (first entry)

XX

DE 151P3D4 cancer gene related HLA peptide #10369.

XX

KW Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoural; cancer;

KW cellular immune response; adenocarcinoma; bladder; colorectal; lung;

KW bronchial; breast; carcinoma; human leukocyte antigen; HLA.

XX

OS Homo sapiens.

XX

PN WO200203860-A2.

XX

PD 24-OCT-2002.

XX

PF 09-APR-2002; 2002WO-US011644.

XX

PR 10-APR-2001; 2001US-0282739P.

PR 25-APR-2001; 2001US-0286630P.

XX

PA (AGEN-) AGENSYN INC.

XX

PT Challita-Eid PM, Raitano AB, Paris M, Hubert RS, Morrison K;

PT Morrison RK, Ge W, Jakobovits A;

XX

DR WPI; 2003-167091/16.

XX

PT New 151P3D4 proteins and genes, useful for eliciting a humoral or

PT cellular immune response, or for diagnosing, prognosis, preventing or

PT treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer

PT or carcinoma.

XX

PS Claim 13; Page 258; 426pp; English.

XX

CC The invention relates to a novel composition comprising a substance that
 CC modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or
 CC a molecule that is modulated by the 151P3D4 protein, where the status of
 CC a cell that expresses the 151P3D4 protein is modulated. The novel
 CC compositions, or the 151P3D4 proteins and genes, are useful for eliciting
 CC a humoral or cellular immune response. The 151P3D4 genes and proteins
 CC are also useful for diagnosing, prognosis, preventing or treating
 CC cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or
 CC bronchial cancer, breast cancer or carcinoma. This sequence represents a
 CC human leukocyte antigen peptide relating to the 151P3D4 composition of
 CC the invention

XX Sequence 10 AA;

QY	2.1%	Score 45;	DB 6;	Length 10;
Best Local Similarity	90.0%;	Pred. No.	9.3e+03;	
Matches	9;	Conservative	1;	Mismatches 0;
		Indels	0;	Gaps 0;

Query Match 2.1%; Score 45; DB 6; Length 10;
 Best Local Similarity 90.0%; Pred. No. 9.3e+03;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 299 VIGIITQGAR 308
 Db ||||| |||||:
 1 VIGIITQGAK 10

Search completed: January 24, 2005, 14:42:22
 Job time : 152 secs

Db 1 ||| 1 | | | 8
 RESULT 3
 ID 012100 PRELIMINARY; PRT; 9 AA.
 AC 012100;
 DT 01-JUL-1997 (TREMBREL_04, Created)
 DT 01-JUL-1997 (TREMBREL_04, Last sequence update)
 DR 01-DEC-2001 (TREMBREL_19, Last annotation update)
 DE Rat protein (Fragment).
 GN Name=rat;
 OC Caprine arthritis encephalitis virus (CAEV).
 OC Viruses; Retroviridae; Lentivirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
 RL Submitted (DEB-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U81441; AAB60836.1; -.
 FT NON_TER 1
 SQ SEQUENCE 9 AA; 922 MW; 21E8644EB7340EBB CRC64;
 Query Match 1.5%; Score 31; DB 2; Length 9;
 Best Local Similarity 62.5%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 11 CGAALICAP 18
 DB 1 ||| 1 | | | 8
 RN [1]
 RESULT 4
 ID 012102 PRELIMINARY; PRT; 9 AA.
 AC 012102;
 DT 01-JUL-1997 (TREMBREL_04, Created)
 DT 01-JUL-1997 (TREMBREL_04, Last sequence update)
 DR 01-DEC-2001 (TREMBREL_19, Last annotation update)
 DE Rat protein (Fragment).
 GN Name=rat;
 OC Caprine arthritis encephalitis virus (CAEV).
 OC Viruses; Retroviridae; Lentivirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
 RL Submitted (DEB-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U81442; AAB60838.1; -.
 FT NON_TER 1
 SQ SEQUENCE 9 AA; 922 MW; 21E8644EB7340EBB CRC64;
 Query Match 1.5%; Score 31; DB 2; Length 9;
 Best Local Similarity 62.5%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 11 CGAALICAP 18
 DB 1 ||| 1 | | | 8
 RN [1]
 RESULT 5
 ID 012104 PRELIMINARY; PRT; 9 AA.
 AC 012104;
 DT 01-JUL-1997 (TREMBREL_04, Created)
 DT 01-JUL-1997 (TREMBREL_04, Last sequence update)
 DR 01-DEC-2001 (TREMBREL_19, Last annotation update)
 DE Rat protein (Fragment).
 GN Name=rat;
 OC Caprine arthritis encephalitis virus (CAEV).
 OC Viruses; Retroviridae; Lentivirus.
 RN [1]
 RP NCBI_TaxID=11660;
 RN [1]
 SEQUENCE FROM N.A.
 RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
 RL Submitted (DEB-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U81443; AAB60840.1; -.
 FT NON_TER 1
 SQ SEQUENCE 9 AA; 922 MW; 21E8644EB7340EBB CRC64;
 Query Match 1.5%; Score 31; DB 2; Length 9;
 Best Local Similarity 62.5%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 11 CGAALICAP 18
 DB 1 ||| 1 | | | 8
 RN [1]
 RESULT 6
 ID OXIA_SQUAC STANDARD; PRT; 9 AA.
 AC P42959;
 DT 01-NOV-1995 (Ref. 32, Created)
 DT 01-NOV-1995 (Ref. 32, Last sequence update)
 DR 05-JUL-2004 (Ref. 44, Last annotation update)
 DE Asparocin (Aspargtocin).
 OS Squalus acanthias (Spiny dogfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Squalidae; Squalidae; Squalidoidae; Squalidae; Squalus.
 OC NCBI_TaxID=7797;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=73031727; PubMed=5083097;
 RA Achér R., Chauvet J., Chauvet M.-T.;
 RT "Phylogeny of the neurohypophyseal hormones. Two new active peptides
 isolated from a cartilaginous fish, *Squalus acanthias*.";
 RL Eur. J. Biochem. 29:12-19(1972).
 RN [2]
 RP SEQUENCE.
 RX MEDLINE=72128038; PubMed=4622083;
 RA Achér R., Chauvet J., Chauvet M.-T., Fontaine M.;
 RT Identification of 2 new neurohypophyseal hormones, valitocin (Val8-
 oxytocin) and asparocin (Asn4-oxytocin) in a selachian fish, the
 RT spiny dog-fish (*Squalus acanthias*).";
 RL C. R. Acad. Sci., D, Sci. Nat. 274:313-316(1972).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the vasopressin/oxytocin family.
 DR InterPro; IPR00081; Neurhyn_P_horm.
 DR Pfam; PF00220; Hormone_4; 1.
 DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
 KW Amidation; Direct protein sequencing; Hormone.
 FT DISULFID 1 6
 MOD RES 9 9 9 Glycine amide.
 FT SEQUENCE 9 AA; 996 MW; 17F83768B44404B CRC64;
 Query Match 1.4%; Score 30; DB 1; Length 9;
 Best Local Similarity 54.5%; Pred. No. 1.8e+06;
 Matches 6; Conservative 1; Mismatches 2; Indels 2; Gaps 1;
 QY 225 CEGNGCAGP 235
 DB 1 ||| 1 | | | 9
 RN [1]
 RESULT 7
 ID QTM4C2 PRELIMINARY; PRT; 10 AA.
 AC QTM4C2;
 DT 01-MAR-2004 (TREMBREL_25, Created)
 DT 01-MAR-2004 (TREMBREL_26, Last sequence update)
 DT 01-MAR-2004 (TREMBREL_26, Last annotation update)
 DR 01-MAR-2004 (TREMBREL_26, Last annotation update)
 DB - Sperm-activating peptide (Tyr-2, Asn-3, Asp-7, 10, Arg-8, Ile-9 SAP-

OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
 OC Scyliorhinidae; Scyliorhinus.
 OC
 NCBI_TaxID=7830;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95062247; PubMed=7972045;
 RA Chauvet J., Rouille Y., Chauveau C., Chauvet M.-T., Acher R.;
 RT "Special evolution of neurohypophysial hormones in cartilaginous fishes: avsotocin and phasavatoxin, two oxytocin-like peptides isolated from the spotted dogfish (Scyliorhinus caniculus).";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).
 CC -- FUNCTION: Displays oxytocic activity on rat uterus.
 CC -- SUBCELLULAR LOCATION: Secreted.
 DR
 PRAM; PF00220; Hormone_4; 1.
 PROSINE; PR00264; NEUROHYPOPHYS HORM; 1.
 DR Amidation; Direct protein sequencing; Hormone.
 FT DISULFID 1 6
 FT MOD RES 9 9
 SQ SEQUENCE 9 AA; 982 MW; 17EBD76B94444B CRC64;
 Oy 225 CLENGCAMPGLG 235
 Db 1 CXYNNC--PVG 9

Query Match 1.3%; Score 27; DB 1; Length 9;
 Best Local Similarity 45.5%; Pred. No. 1.8e+06; Mismatches 2; Indels 2; Gaps 1;
 Matches 5; Conservative 2;

RESULT 12
 07M4Q9
 ID 07M4Q9 PRELIMINARY; PRT; 9 AA.
 AC 07M4Q9;
 DT 01-MAR-2004 (TREMBLrel. 26, Created)
 DT 01-MAR-2003 (TREMBLrel. 25, Last sequence update)
 DR Octamer-binding protein, Ku-like, 83K chain (Fragment).
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91131605; PubMed=1993678;
 RA May G.; Sutton C.; Gould H.;
 RT "Purification and characterization of Ku-2, an octamer-binding protein related to the autoantigen Ku.";
 RL J. Biol. Chem. 266:3052-3059(1991).
 DR PIR; B39504; B39504.
 FT NON_TER 9
 SQ SEQUENCE 9 AA; 1096 MW; C65D4AAB144699D2 CRC64;

Query Match 1.3%; Score 27; DB 2; Length 9;
 Best Local Similarity 80.0%; Pred. No. 1.8e+06; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 1;

RESULT 13
 FAR2 ASCSU STANDARD; PRT; 7 AA.
 ID FAR2 ASCSU
 AC P31890;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE FMRFamide-like neuropeptide AR2.
 OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides), and

OS panagrellus redivivus
 OC Eukaryota; Metazoa; Chromadorea; Ascaridida; Ascaridoidea;
 OC Ascarididae; Ascaris.
 NCBI_TaxID=6253, 6233;
 RN [1]
 RP SEQUENCE.
 RX SPECIES=A.suum;
 RC SPECIES=P.redivivus;
 RX MEDLINE=93324431; PubMed=83132542;
 RA Cowden C., Stretton A.O.W.;
 RT Maule A.G.; Shaw C.; Bowman J.W.;
 RR "AF2, an Ascaris neuropeptide: isolation, sequence, and bioactivity.>";
 RL Peptides 14:423-430(1993).
 RN [2]
 RP SEQUENCE.
 RX SPECIES=P.redivivus;
 RC SPECIES=P.redivivus;
 RX MEDLINE=95060998; PubMed=7970891;
 RA Maule A.G.; Shaw C.; Bowman J.W.;
 RR "The FMRFamide-like neuropeptide AF2 (Ascaris suum) is present in the free-living nematode, Panagrellus redivivus (Nematoda, Rhabditida).";
 RL Parasitology 109:351-356(1994).
 CC -- FUNCTION: Has effects on muscle tension.
 CC -- SUBCELLULAR LOCATION: Secreted.
 CC -- TISSUE SPECIFICITY: Found in the nerve cords and a variety of ganglia particularly in the anterior regions.
 CC -- SIMILARITY: Belongs to the FAR2 (FMRFamide-related peptide) family.
 CC Anidation; Direct protein sequencing; Neuropeptide.
 FT MOD RES 7 7
 SQ SEQUENCE 7 AA; 992 MW; 69D4073B5B11B350 CRC64;
 Oy 152 HEVTK 156
 Db 2 HEVLR 6

RESULT 14
 PK2 PERAM
 ID PK2 PERAM STANDARD; PRT; 8 AA.
 AC P82686;
 DT 05-JUL-2004 (Rel. 44, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DR 05-JUL-2004 (Rel. 44, Last annotation update)
 DS Kinin-2 (Pea-K-2).
 OS Periplaneta americana (American cockroach)
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
 OC Blattidae; Periplaneta.
 RN [1]
 RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.
 RC TISSUE-Corpora cardiaca; Blattaria; Blattoidea;
 RX MEDLINE=98010462; PubMed=9350919;
 RA Prede R., Kellner R., Rapus J., Penzlin H., Gade G.;
 RR "Isolation and structural elucidation of eight kinins from the retrocerebral complex of the American cockroach, Periplaneta americana.>";
 RT Regul. Pept. 71:199-205(1997).
 RL
 CC -- FUNCTION: Mediates visceral muscle contractile activity (myotropic activity).
 CC -- SUBCELLULAR LOCATION: Secreted.
 CC -- MASS SPECTROMETRY: MW=855.04; METHOD=Electrospray; RANGE=1-8;
 CC -- NOTE=Ref. 1
 CC -- SIMILARITY: Belongs to the kinin family.
 CC
 KW Amidation; Direct protein sequencing; Neuropeptide.
 FT MOD RES 8 8
 SQ SEQUENCE 8 AA; 856 MW; DC6365ASB99SBDDA CRC64;
 Oy 122 NDDNP 126
 Db 5 NDDNP 9

Query Match 1.2%; Score 26; DB 1; Length 8;
 Best Local Similarity 42.9%; Pred. No. 1.8e+06; Mismatches 3; Indels 0; Gaps 0;

Qy 250 SSYKTIWG 256
 : : | : |
 Db 2 ASFSSWIG 8

RESULT 15

TALL_PICJA STANDARD; PRT; 9 AA.

ID AC PI7470; DT 01-AUG-1990 (Rel. 15, Created)
 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Transaldolase I (EC 2.2.1.2) (Fragment).
 OS Pichia Jadinii (Yeast) (Candida utilis).
 OC Eukaryota; Fungi; Ascomycota; Saccharomyctina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Pichia.
 OX NCBI_TaxID:4903;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=77110646; PubMed=556924;
 RA Sun S. C., Joris L., Toulas O.;
 RT "Purification of crystallization of transaldolase isozyme I and III in Candida
 utilis", Arch. Biophys. 178:69-78(1977).
 RT evidence for different genetic origin of isozymes I and III in Candida
 utilis.", Arch. Biophys. 178:69-78(1977).
 CC -!- FUNCTION: Transaldolase is important for the balance of
 metabolite in the pentose-phosphate pathway.
 CC -!- CATALYTIC ACTIVITY: Sedoheptulose 7-phosphate + D-fructose 6-phosphate
 CC 3-phosphate = D-ribose 5-phosphate + D-glyceraldehyde.
 CC -!- PATHWAY: Pentose phosphate pathway; nonoxidative part.
 CC -!- SIMILARITY: Belongs to the transaldolase family. Subfamily 1.
 DR IPR01585; A12872; A12872.
 DR InterPro; IPR01585; Transaldolase.
 DR PROSITE; PS01054; TRANSALDOLASE_1; PARTIAL.
 DR PROSITE; PS00958; TRANSALDOLASE_2; PARTIAL.
 KW Direct protein sequencing; Pentose shunt; Transferase.
 FT NON_TER 1 1
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1008 MW; 274F31AF0BB1E058 CRC64;

Query Match 1.2%; Score 26; DB 1; Length 9;
 Best Local Similarity 66.7%; Pred. No 1.8e+06;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 63 GHICET 68
 Db 2 GHICBT 7

Search completed: January 24, 2005, 14:39:44
 Job time : 193 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: January 24, 2005, 14:36:23 ; Search time 39 seconds
(without alignments)

Title: Perfect score: US-09-744-804A-78
Sequence: 1 MPRPLLAALGALLCAPSL.....RILPVAWHNRIALRBLIGC.387

Scoring table: BL05Un62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1102

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

RESULT 1

Query: E8394
Species: Bos primigenius taurus (cattle)
C Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997
C Accession: E48394
R. Mather, I.H.; Banghart, L.R.; Lane, W.S.
Biochem. Mol. Biol. Int. 29, 555-554, 1993

A Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig T-cell-like sequences.

A Reference number: A48394; MUID:93250576; PMID:8485470

A Status: preliminary

A Molecule type: protein

A Residues: 1-7 <MAT>

A Experimental source: milk
A Note: sequence extracted from NCBI backbone (NCBIP:131450)

Keywords:

Query Match %
Score 36; DB 2; Length 7;
Best Local Similarity 85.7%; Pred. No. 2.8e+05; Mismatches 1; Indels 0; Gaps 0;
Matches 6; Conservative 0;

Description
Query Match %
Score 36; DB 2; Length 7;
Best Local Similarity 85.7%; Pred. No. 2.8e+05; Mismatches 1; Indels 0; Gaps 0;
Matches 6; Conservative 0;

RESULT 2

Query: QY 101 WPELAR 107
DB 1 WAPELAR 7

Query Match %
Score 36; DB 2; Length 7;
Best Local Similarity 85.7%; Pred. No. 2.8e+05; Mismatches 1; Indels 0; Gaps 0;

Description
Query Match %
Score 36; DB 2; Length 7;
Best Local Similarity 85.7%; Pred. No. 2.8e+05; Mismatches 1; Indels 0; Gaps 0;

RESULT 3

Query: QY 101 WPELAR 107
DB 1 WAPELAR 7

Query Match %
Score 36; DB 2; Length 7;
Best Local Similarity 85.7%; Pred. No. 2.8e+05; Mismatches 1; Indels 0; Gaps 0;

Description
Query Match %
Score 36; DB 2; Length 7;
Best Local Similarity 85.7%; Pred. No. 2.8e+05; Mismatches 1; Indels 0; Gaps 0;

RESULT 4

Query: QY 101 WPELAR 107
DB 1 WAPELAR 7

Query Match %
Score 36; DB 2; Length 7;
Best Local Similarity 85.7%; Pred. No. 2.8e+05; Mismatches 1; Indels 0; Gaps 0;

Description
Query Match %
Score 36; DB 2; Length 7;
Best Local Similarity 85.7%; Pred. No. 2.8e+05; Mismatches 1; Indels 0; Gaps 0;

Query Match %
Score 36; DB 2; Length 7;
Best Local Similarity 85.7%; Pred. No. 2.8e+05; Mismatches 1; Indels 0; Gaps 0;

Db 1 WOPELAR 7

P;8/Modified site: amidated carboxyl end (Gly) #status experimental

RESULT 3
 Glycoprotein component 15/major fat-globule membrane protein/MFG-E8 homolog - bovine (fr
 C;Species: Bos primigenius taurus (cattle)
 C;Accession: H4394 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997

A;Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig
 II-like sequences.
 A;Reference number: A4394; MUID:93250576; PMID:8485470

A;Accession: H4394 #sequence_revision 12-Feb-1998 #text_change 07-May-1999

A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-6 <MAY>

A;Experimental source: milk
 A;Note: sequence extracted from NCBI backbone (NCBIP:131518)

C;Keywords: glycoprotein

Query Match 1.4%; Score 29; DB 2; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2.8e+05;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
 sperm-activating peptide (Tyr-2, Asn-3, Asp-7-10, Arg-8, Ile-9 SAP-1) - Echinometra math

C;Accession: G60589
 C;Species: Echinometra mathaei
 C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-2004

C;Yoshimura, K. I.; Kajura, H.; Nomura, K.; Takeo, T.; Shimomishi, Y.; Kurita, M.; Yamaguc

Comp. Biochem. Physiol. B 94, 739-751, 1989

A;Title: A halogenated amino acid-containing sperm activating peptide and its related pe

ctus nudus, Echinometra mathaei and Heterocentrotus mammillatus.

A;Reference number: A60527

A;Accession: G60589

A;Molecule type: protein
 A;Residues: 1-10 <YOS>

A;Cross-references: UNIPROT:Q7M4C2

Query Match 1.4%; Score 29; DB 2; Length 10;
 Best Local Similarity 55.6%; Pred. No. 1e+04;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Db 1 YSLNGHEFD 170
 2 YNLNGDRID 10

RESULT 5
 JS0316

leucokinin VI - Madeira cockroach
 C;Species: Leucophaea madeirea (Madeira cockroach)

C;Accession: JS0316 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004

A;Accession: JS0316 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004

A;Residues: 1-8 <HOL>

A;Cross-references: UNIPROT:P1998

C;Comments: Leucokinins, a family of cephalomyotrophic peptides, stimulate contractile act

C;Keywords: amidated carboxyl end; cephalomyotrophic peptide; pyroglutamic acid
 P;1;Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 1.3%; Score 28; DB 2; Length 8;
 Best Local Similarity 57.1%; Pred. No. 2.8e+05; Mismatches 1; Indels 0; Gaps 0;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 1 SSFHSG 8

Query Match 1.3%; Score 25; DB 2; Length 8;
 Best Local Similarity 57.1%; Pred. No. 2.8e+05; Mismatches 1; Indels 0; Gaps 0;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 2 SSFHSG 8

RESULT 6
 S65385

Cytochrome-c oxidase (EC 1.9.3.1) chain VII, hepatic - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Accession: S65385 #sequence_revision 20-Feb-1998 #text_change 07-May-1999

C;Y-Schaeffer, H.; Noack, H.; Halangk, W.; Brandt, U.; von Jagow, G.

Biochem. 230, 231-241, 1995

A;Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-termini

A;Reference number: S65372; MUID:95324529; PMID:7601105

A;Accession: S65385

A;Status: preliminary

A;Molecule type: protein
 A;Residues: 1-10 <SCH>

A;Keywords: oxidoreductase

Query Match 1.3%; Score 28; DB 2; Length 10;
 Best Local Similarity 57.1%; Pred. No. 1.2e+04; Mismatches 1; Indels 0; Gaps 0;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 1 NKVPEKQ 9

RESULT 7
 B39504

Octamer-binding protein, Ku-like, 83K chain - human (fragment)

C;Species: Homo sapiens (man)

C;Accession: B39504 #sequence_revision 30-Dec-1991 #text_change 09-Jul-2004

C;Y-May, G.; Sutton, C.; Gould, H.

J. Biol. Chem. 266, 3052-3059, 1991

A;Title: Purification and characterization of Ku-2, an octamer-binding protein related to

A;Reference number: A39504; MUID:9131605; PMID:1993678

A;Accession: B39504

A;Status: preliminary

A;Molecule type: protein
 A;Residues: 1-9 <MAY>

A;Cross-references: UNIPROT:Q7M4Q9

Query Match 1.3%; Score 27; DB 2; Length 9;
 Best Local Similarity 80.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 NDDNP 126

2 NEDNP 9

RESULT 8
 A12872

transaldolase (EC 2.2.1.2) I - Yeast (Pichia jadinii) (fragment)

C;Species: Pichia jadinii, Candida utilis

C;Accession: A12872 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004

C;Y-Sun, S.C.; Joris, L.; Tsolas, O.

Arch. Biochem. Biophys. 178, 69-78, 1977

A;Title: Purification and crystallization of transaldolase isozyme I and evidence for dif

A;Reference number: A12872; MUID:7710646; PMID:556924

A;Accession: A12872

A;Molecule type: protein

A;Residues: 1-9 <SUN>
 A;Cross-references: UNIPROT:PI17440
 C;Keywords: transfrase

 Query Match 1.2%; Score 26; DB 2; Length 9;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 63 GRNCET 68
 Db 2 GRHCBT 7

RESULT 9
 PX0030 triacylglycerol lipase (EC 3.1.1.3) II - yeast (Geotrichum candidum) (fragments)
 C;Species: Geotrichum candidum
 C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
 C;Accession: PX0030
 R;Sugihara, A.; Shimada, Y.; Tominaga, Y.
 J;Bichsel, 107, 426-430, 1990
 A;Title: Separation and characterization of two molecular forms of Geotrichum candidum 1
 A;Reference number: PX0030; MUID:90256718; PMID:2341377
 A;Accession: PX0030
 A;Molecule type: protein
 A;Residues: 1-10 <SUG>
 A;Cross-references: UNIPROT:P22394
 C;Comment: Lipase catalyzes the hydrolysis of triacylglycerols. This fungus contains two
 C;Keywords: carboxylic ester hydrolase

Query Match 1.2%; Score 26; DB 2; Length 10;
 Best Local Similarity 83.3%; Pred. No. 1.7e+04;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PRPLL 7
Db 3 PRXL 8

RESULT 10
 JH0253 gut pentapeptide - Japanese eel
 C;Species: Anguilla japonica (Japanese eel)
 C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1995
 C;Accession: JH0253
 R;Uesaka, T.; Ikeda, T.; Kubota, I.; Muneoka, Y.; Ando, M.
 J;Biochem. Biophys. Res. Commun. 180, 828-832, 1991
 A;Title: Structure and function of a pentapeptide isolated from the gut of the eel.
 A;Reference number: JH0253; MUID:92062113; PMID:1953755
 A;Accession: JH0253
 A;Molecule type: protein
 A;Residues: 1-5 <UES>
 A;Experimental source: gut
 C;Comment: This peptide increased basal tone of the circular muscle of the esophagogastric and of the circular muscle of the gastro-intestinal junction.

Query Match 1.2%; Score 25; DB 2; Length 5;
 Best Local Similarity 80.0%; Pred. No. 2.8e+05;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 184 GWNK 188
Db 1 GWNK 5

RESULT 11
 PR0691 T-cell receptor beta chain V-D-J region (154-2K) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C;Accession: PR0691
 R;Feeley, A.J.
 J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A;Reference number: PR0509; MUID:91277601; PMID:1711558
 A;Accession: PR0691
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-8 <FEE>
 A;Experimental source: day 18 fetal thymus, strain BALB/C
 C;Keywords: T-cell receptor

RESULT 12
 S19288 acylase - Kluvera cryocrescens
 C;Species: Kluvera cryocrescens
 C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
 C;Accession: S19288
 R;Martin, J.; Slade, A.; Aitken, A.; Arche, R.; Virden, R.
 J;Biochem. J. 280, 659-662, 1991
 A;Title: Chemical modification of serine at the active site of penicillin acylase from Kluvera cryocrescens
 A;Reference number: S19288; MUID:92109664; PMID:1764029
 A;Accession: S19288
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-8 <MAR>
 A;Cross-references: UNIPROT:Q7M124

Query Match 1.2%; Score 25; DB 2; Length 8;
 Best Local Similarity 80.0%; Pred. No. 2.8e+05;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 136 MWVIG 140
Db 3 MWVIG 7

RESULT 13
 JS0315 leucokinin V - Madeira cockroach
 C;Species: Leucophaeamaderae (Madeira cockroach)
 C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
 C;Accession: JS0315
 R;Holman, G.M.; Cook, B.J.; Nachman, R.J.
 J;Comp. Biochem. Physiol. C 88, 27-30, 1987
 A;Title: Isolation, primary structure, and synthesis of leucokinins V and VI: myotrophic I
 A;Reference number: JS0315
 A;Accession: JS0315
 A;Molecule type: protein
 A;Residues: 1-8 <HOL>
 A;Cross-references: UNIPROT:PI19987
 C;Comment: Leucokinins, a family of cephalomyotrophic peptides, stimulate contractile acti
 C;Keywords: amidated carboxyl end, cephalomyotrophic peptide
 F/B/Modified site: amidated carboxyl end (GLY) #status experimental

Query Match 1.2%; Score 25; DB 2; Length 8;
 Best Local Similarity 42.9%; Pred. No. 2.8e+05;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 250 SSYKTVG 256
Db 2 SGSSWQ 8

RESULT 14
 A1117 acetylcholinesterase (EC 3.1.1.7), venom - Asian cobra (fragment)

C;Species: Naja naja oxiana (Asian cobra Oxus cobra)
 C;Date: 27-Mar-1992 #sequence_revision 27-Mar-1992 #text_change 09-Jul-2004
 C;Accession: A41117
 C;Kreikenkamp, H.J.; Weise, C.; Raba, R.; Aviisaar, A.; Hucho, F.
 Proc. Natl. Acad. Sci. U.S.A. 88, 6117-6121, 1991
 A;Title: Anionic subsites of the catalytic center of acetylcholinesterase from Torpedo a
 A;Reference number: A41117; MUID:91296772; PMID:2068091
 A;Accession: A41117
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-8 <KRE>
 A;Cross-references: UNIPROT:Q7LU27
 C;Keywords: carboxylic ester hydrolase

Query Match 1.2%; Score 25; DB 2; Length 8;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 262 WNPW 265
 Db 5 WNPW 8

RESULT 15

S07241 litorin - Rohde's leaf frog

C;Species: Phylomedusa rohdei (Rohde's leaf frog)

C;Date: 12-Feb-1993 #sequence_revision 12-Mar-1993 #text_change 09-Jul-2004

C;Accession: S07241
 R;Barra, D.; Falconieri Espanier, G.; Simmaco, M.; Bossa, F.; Melbiorri, P.; Espanier, F.; FERS Lett. 182, 53-56, 1985

A;Title: Rohdei-litorin, a new peptide from the skin of Phylomedusa rohdei.

A;Reference number: S07241; MUID:85127560; PMID:3838283

A;Accession: S07241

A;Molecule type: protein

A;Residues: 1-9 <BAR>

A;Cross-references: UNIPROT:P08946

C;Superfamily: gastrin-releasing peptide

C;Keywords: amidated carboxyl end; blocked amino end; neuropeptide; pyroglutamic acid

F;1;Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;9;Modified site: amidated carboxyl end (Met) #status experimental

Query Match 1.2%; Score 25; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy 135 RMWVWG 140
 Db 1 QLWATG 6

Search completed: January 24, 2005, 14:46:21
 Job time : 40 secs

RESULT 2
 US-09-865-548A-43
 ; Sequence 43, Application US/09865548A
 ; Publication No. US20030096298A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Barnea, Eilon
 ; APPLICANT: Ziv, Tamar
 ; ACTION: Arie
 ; TITLE OF INVENTION: PEPTIDES IDENTIFIED THEREBY AND THEIR USES
 ; FILE REFERENCE: 01/22060
 ; CURRENT APPLICATION NUMBER: US/09/865, 548A
 ; CURRENT FILING DATE: 2001-05-16
 ; PRIOR APPLICATION NUMBER: US 60/290, 958
 ; PRIOR FILING DATE: 2001-05-16
 ; NUMBER OF SEQ ID NOS: 204
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 43
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic peptide
 ; US-09-865-548A-43

Query Match 2.1%; Score 44; DB 10; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.5e+06; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 ALICAPSLL 21
 Db 1 ALICAPSLL 9

RESULT 3
 US-10-235-852-19
 ; Sequence 19, Application US/10235852
 ; Publication No. US2004005298A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gazi, End
 ; TITLE OF INVENTION: PEPTIDES AND METHODS USING SAME FOR DIAGNOSING AND TREATING AMYLOID
 ; FILE REFERENCE: 02/13654
 ; CURRENT APPLICATION NUMBER: US/10/235, 852
 ; CURRENT FILING DATE: 2002-09-06
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 19
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Lactadherin derived, active site sequence
 ; US-10-235-852-19

Query Match 1.9%; Score 41; DB 15; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.5e+06; Mismatches 0; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 309 NFGSVOFV 316
 Db 1 NFGSVOFV 8

RESULT 4
 US-09-908-322-88
 ; Sequence 88, Application US/09908322
 ; Patent No. US20020107194A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ish-Horowicz, David
 ; APPLICANT: Henrique, Domingos Manuel Pinto
 ; APPLICANT: Lewis, Julian Hart
 ; APPLICANT: Artavanis-Tsakonas, Spyridon
 ; FEATURE:
 ; OTHER INFORMATION: Lactadherin derived, active site sequence
 ; US-09-908-322-88

Query Match 1.9%; Score 41; DB 15; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.5e+06; Mismatches 0; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 309 NFGSVOFV 316
 Db 1 NFGSVOFV 8

RESULT 5
 US-09-783-931-88
 ; Sequence 88, Application US/09783931
 ; Publication No. US20030073620A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ish-Horowicz, David
 ; APPLICANT: Henrique, Domingos Manuel Pinto
 ; APPLICANT: Lewis, Julian Hart
 ; APPLICANT: Artavanis-Tsakonas, Spyridon
 ; FEATURE:
 ; OTHER INFORMATION: Lactadherin derived, active site sequence
 ; US-09-783-931-88

Query Match 1.8%; Score 39; DB 9; Length 8;
 Best Local Similarity 85.7%; Pred. No. 1.5e+06; Mismatches 1; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 30 NPCKNGG 36
 Db 1 NPCKNGG 7

RESULT 6
 US-09-908-322-88
 ; Sequence 88, Application US/09908322
 ; Patent No. US20020107194A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ish-Horowicz, David
 ; APPLICANT: Henrique, Domingos Manuel Pinto
 ; APPLICANT: Lewis, Julian Hart
 ; APPLICANT: Artavanis-Tsakonas, Spyridon
 ; FEATURE:
 ; OTHER INFORMATION: Lactadherin derived, active site sequence
 ; US-09-908-322-88

Query Match 1.8%; Score 39; DB 9; Length 8;
 Best Local Similarity 85.7%; Pred. No. 1.5e+06; Mismatches 1; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 30 NPCKNGG 36
 Db 1 NPCKNGG 7

RESULT 7
 US-09-783-931-88
 ; Sequence 88, Application US/09783931
 ; Publication No. US20030073620A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ish-Horowicz, David
 ; APPLICANT: Henrique, Domingos Manuel Pinto
 ; APPLICANT: Lewis, Julian Hart
 ; APPLICANT: Artavanis-Tsakonas, Spyridon
 ; FEATURE:
 ; OTHER INFORMATION: Lactadherin derived, active site sequence
 ; US-09-783-931-88

Query Match 1.8%; Score 39; DB 9; Length 8;
 Best Local Similarity 85.7%; Pred. No. 1.5e+06; Mismatches 1; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 30 NPCKNGG 36
 Db 1 NPCKNGG 7

RESULT 8
 US-09-744-804a-78
 ; Sequence 88, Application US/09908322
 ; Patent No. US20020107194A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ish-Horowicz, David
 ; APPLICANT: Henrique, Domingos Manuel Pinto
 ; APPLICANT: Lewis, Julian Hart

Artavanis-Tsakonas, Spyridon
 Gray, Grace
 ADDRESSE: Pennie & Edmonds LLP
 STREET: 115 Avenue of the Americas
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10036/2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette

Aravanis-Tsakonas, Spyridon
 Gray, Grace
 TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF VERTEBRATE DELTA GENE AND METHODS BASED THEREON
 NUMBER OF SEQUENCES: 94
 CORRESPONDENCE ADDRESS:
 ADDRESSE: Pennie & Edmonds LLP
 STREET: 115 Avenue of the Americas
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10036/2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 08/981, 392
 FILING DATE: 22-DEC-1997
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/981, 392
 FILING DATE: 17-JUL-2001
 ATTORNEY/AGENT INFORMATION:
 NAME: Mirock, S Leslie
 REGISTRATION NUMBER: 18,872
 INFORMATION FOR SEQ ID NO: 88:
 REFERENCE/DOCKET NUMBER: 7326-123
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-790-9090
 TELEFAX: 212-869-8864
 TELEX: 66141 PENNIE
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 88:
 US-09-908-322-88

Query Match 1.8%; Score 39; DB 9; Length 8;
 Best Local Similarity 85.7%; Pred. No. 1.5e+06; Mismatches 1; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 30 NPCKNGG 36
 Db 1 NPCKNGG 7

RESULT 9
 US-09-744-804a-78
 ; Sequence 88, Application US/09908322
 ; Publication No. US20020107194A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ish-Horowicz, David
 ; APPLICANT: Henrique, Domingos Manuel Pinto
 ; APPLICANT: Lewis, Julian Hart
 ; APPLICANT: Artavanis-Tsakonas, Spyridon
 ; FEATURE:
 ; OTHER INFORMATION: Lactadherin derived, active site sequence
 ; US-09-744-804a-78

Query Match 1.8%; Score 39; DB 9; Length 8;
 Best Local Similarity 85.7%; Pred. No. 1.5e+06; Mismatches 1; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 30 NPCKNGG 36
 Db 1 NPCKNGG 7

RESULT 10
 US-09-744-804a-78
 ; Sequence 88, Application US/09908322
 ; Patent No. US20020107194A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ish-Horowicz, David
 ; APPLICANT: Henrique, Domingos Manuel Pinto
 ; APPLICANT: Lewis, Julian Hart

Artavanis-Tsakonas, Spyridon
 Gray, Grace
 ADDRESSE: Pennie & Edmonds LLP
 STREET: 115 Avenue of the Americas
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10036/2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/783,931
 FILING DATE: 15-Feb-2001
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/981,392
 FILING DATE: 22-DEC-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Antler, Adriane M.
 REGISTRATION NUMBER: 32,605
 REFERENCE/DOCKET NUMBER: 7326-122
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-790-8869
 TELEFAX: 212-869-8864
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 88:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: peptide
 STRANGENESS: <Unknown>
 MOLECULE TYPE: peptide
 TOPOLOGY: unknown
 SEQUENCE DESCRIPTION: SEQ ID NO: 88:
 ; US-09-783-931-88

Query Match 1.8%; Score 39; DB 10; Length 8;
 Best Local Similarity 85.7%; Pred. No. 1.5e+06; Mismatches 6; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 30 NICHNGG 36
 Db 1 NPCKNGG 7

RESULT 6

US-10-743-649-6

Sequence 6, Application US/10743639
 Publication No. US20040208849A1
 ; GENERAL INFORMATION:
 ; PUBLICATION NO. US20040170607A1
 ; APPLICANT: PRO-VIRUS, INC.
 ; TITLE OF INVENTION: ONCOLYTIC VIRUS
 ; FILE REFERENCE: 2370-63
 ; CURRENT APPLICATION NUMBER: US/10/743,649
 ; CURRENT FILING DATE: 2003-12-22
 ; PRIORITY APPLICATION NUMBER: US/09/644,444
 ; PRIORITY FILING DATE: 2000-09-18
 ; PRIORITY APPLICATION NUMBER: 09/397,873
 ; PRIORITY FILING DATE: 1999-09-17
 ; NUMBER OF SEQ ID NOS: 52
 ; SOFTWARE: Patentin Ver. 2.1
 ; OTHER INFORMATION: peptide

Qy 348 WDNHSH 353
 Db 2 WDNHSH 7

RESULT 8

US-09-572-404B-3564

Sequence 8, Application US/09572404B
 Publication No. US20030078374A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Protein Ltd
 ; TITLE OF INVENTION: Complementary peptide ligands from the human genome
 ; FILE REFERENCE: Human Patent
 ; CURRENT APPLICATION NUMBER: US/09/572,404B
 ; CURRENT FILING DATE: 2000-05-17
 ; NUMBER OF SEQ ID NOS: 4203
 ; SOFTWARE: ProPatent version 1.0
 ; SEQ ID NO 3564
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 ; FEATURE:
 ; OTHER INFORMATION: sequence located in NID2 at 780-789 and may interact with Sequence
 ; OTHER INFORMATION: in this patent.

US-09-572-404B-3564

Query Match 1.7%; Score 35; DB 10; Length 10;
 Best Local Similarity 83.3%; Pred. No. 1.4e+04; Mismatches 5; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 52 SYTCSC 57
 Db 5 SYTCSC 10

RESULT 9

US-09-947-925A-29

Sequence 9, Application US/09947925A
 ; Publication No. US2005548A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Huber, Brian
 ; APPLICANT: Richards, Cynthia
 ; TITLE OF INVENTION: Molecular Constructs Containing a Carcinoembryonic
 ; TITLE OF INVENTION: Antigen Regulatory
 ; FILE REFERENCE: PBL087U3

Qy 348 WDNHSH 353
 Db 2 WDNHSH 7

RESULT 7

US-10-743-649-6

Query Match 1.7%; Score 35; DB 16; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.5e+05; Mismatches 4; Indels 0; Gaps 0;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 348 WDNHSH 353
 Db 2 WDNHSH 7

RESULT 7

US-10-743-639-6

US-10-083-768-59

CURRENT APPLICATION NUMBER: US/09/947,925A
 CURRENT FILING DATE: 2001-09-06
 PRIOR APPLICATION NUMBER: US/08/154,712
 PRIOR FILING DATE: 1993-11-19
 NUMBER OF SEQ ID NOS: 36
 SOFTWARE: Patentin version 3.0
 SEQ ID NO: 29
 LENGTH: 8
 TYPE: PRT
 ORGANISM: consensus sequence
 FEATURE:
 NAME/KEY: msc feature
 OTHER INFORMATION: consensus sequence F6 from transcriptional dictionary
 Best Local Similarity 46.7%; Pred. No. 1.5e+06; 1; Mismatches 1; Indels 6; Gaps 1;
 Matches 7; Conservative 1;
 OTHER INFORMATION: of Locker a
 OTHER INFORMATION: nd Buzard (1990).
 US-09-947-925A-29

RESULT 10

Query Match 1.6%; Score 34; DB 9; Length 8;
 Best Local Similarity 71.4%; Pred. No. 1.5e+05; 2; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 2;
 Qy 211 SHTACT 217
 Db :|||: 1 TENTACT 7

US-10-083-768-69

; Sequence 69, Application US/10083768
 ; Publication No. US20030158116A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dower, William J.
 ; Barrett, Ronald W.
 ; Cwirla, Steven E.
 ; Duffin, David J.
 ; Gates, Christian
 ; Haselden, Sherril S.
 ; Mattheakis, Larry C.
 ; Schatz, Peter J.
 ; Wagstrom, Christopher R.
 ; Wrighton, Nicholas C.
 ; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
 ; THROMBOPOIETIN RECEPTOR
 ; NUMBER OF SEQUENCES: 232
 ; CORRESPONDENCE ADDRESS:
 ; STREET: Five Moore Drive, P. O. Box 13398
 ; CITY: Research Triangle Park
 ; STATE: NC
 ; COUNTRY: USA
 ; ZIP: 27709
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: FLOPPY DISK
 ; COMPUTER: IBM PC COMPATIBLE
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/083,768
 ; FILING DATE: 27-Feb-2002
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hrubec, Robert T.
 ; REGISTRATION NUMBER: 36,392
 ; REFERENCE/DOCKET NUMBER: PK3065USW
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 919-248-1000
 ; INFORMATION FOR SEQ ID NO: 69:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 9 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: <Unknown>
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: Peptide
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 69:

RESULT 11

Query Match 1.6%; Score 34; DB 14; Length 9;
 Best Local Similarity 46.7%; Pred. No. 1.5e+06; 1; Mismatches 1; Indels 6; Gaps 1;
 Matches 7; Conservative 1;
 Qy 216 CTTRFELGCGLNGC 230
 Db :|||: 1 CTLEF----MNGC 9

US-10-393-269-38

; Sequence 38, Application US/10393269
 ; Publication No. US20030223979A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GELLERFORS, Par
 ; TITLE OF INVENTION: NEW THERAPEUTIC METHOD FOR TREATING PATIENTS WITH ACUTE
 ; TITLE OF INVENTION: INTERMITTENT PORPHYRIA (AIP) AND OTHER PORPHYRIC
 ; FILE REFERENCE: GELLERFORS-1A
 ; CURRENT APPLICATION NUMBER: US/10/393,269
 ; PRIOR FILING DATE: 2003-03-21
 ; NUMBER OF SEQ ID NOS: 40
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO: 38
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE: Description of Artificial Sequence: encoded by
 ; OTHER INFORMATION: SEQ ID NO:37
 ; US-10-393-269-38

Query Match 1.6%; Score 34; DB 14; Length 9;
 Best Local Similarity 57.1%; Pred. No. 1.5e+06; 2; Mismatches 1; Indels 0; Gaps 0;
 Matches 4; Conservative 2;
 Qy 372 VAWHNR 378
 Db :|||: 3 MGWHNRV 9

RESULT 12

US-10-774-176-15

; Sequence 16, Application US/10774176
 ; Publication No. US/0040265275A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CARROLL, MILES WILLIAM
 ; APPLICANT: MYERS, KEVIN ALAN
 ; TITLE OF INVENTION: POLYPEPTIDE
 ; FILE REFERENCE: 07883/0120
 ; CURRENT APPLICATION NUMBER: US/10/774,176
 ; CURRENT FILING DATE: 2004-02-06
 ; PRIOR APPLICATION NUMBER: US/09/533,798
 ; PRIOR FILING DATE: 2000-03-24
 ; PRIOR APPLICATION NUMBER: 60/126,187
 ; PRIOR FILING DATE: 1998-03-25
 ; PRIOR APPLICATION NUMBER: 60/126,188
 ; PRIOR FILING DATE: 1999-03-25
 ; PRIOR APPLICATION NUMBER: GB 9825303.2
 ; PRIOR FILING DATE: 1998-11-18
 ; PRIOR APPLICATION NUMBER: GB 9901739.4
 ; PRIOR FILING DATE: 1999-01-27
 ; PRIOR APPLICATION NUMBER: GB 9917995.4
 ; PRIOR FILING DATE: 1999-07-30
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: Patentin version 2.1
 ; SEQ ID NO: 16
 ; LENGTH: 9

```

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 5T4 9 Mer
; US-10-774-176-16

Query Match          1.6%; Score 34; DB 17; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.5e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Oy      123 DDNPWII 128
Db      3 DNNPWW 8

RESULT 13
US-09-935-430-433
; Sequence 433, Application US/09935430
; Publication No. US2003001466A1
; GENERAL INFORMATION:
; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAF, DANIEL
; APPLICANT: LEVIN, BLANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOWITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51:58-20050.00
; CURRENT APPLICATION NUMBER: US/09/935, 430
; CURRENT FILING DATE: 2001-08-22
; PRIORITY APPLICATION NUMBER: 60/227, 098
; PRIORITY FILING DATE: 2000-08-22
; PRIORITY APPLICATION NUMBER: 60/282, 739
; PRIORITY FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 433
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
; US-09-935-430-433

Query Match          1.6%; Score 34; DB 10; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.7e+04;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Oy      96 LGIQLQWVPEL 105
Db      1 VGLQQWQKL 10

RESULT 14
US-09-809-638-585
; Sequence 585, Application US/09809638
; Publication No. US20030059895A1
; GENERAL INFORMATION:
; APPLICANT: Mary Paris
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Daniel E. H. Araf
; APPLICANT: Arthur B. Raitano
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 125P5C8: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN VARIOUS CANCERS
; FILE REFERENCE: 129_35US01
; CURRENT APPLICATION NUMBER: US/09/809, 638
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 746
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 680
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-809-638-680

Query Match          1.6%; Score 34; DB 10; Length 10;
Best Local Similarity 55.6%; Pred. No. 1.7e+04;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Oy      249 SSSYKHWGL 257
Db      1 STRYHWWGI 9

Search completed: January 24, 2005, 14:44:51
Job time : 144 SECs

CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 746

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OM protein - protein search, using sw model
Run on: January 24, 2005, 14:36:23 ; Search time 40 Seconds
Title: US-09-744-804A-78
Perfect score: 2110
Sequence: MPPRPLIAGCGAGLCAPL. RILPVAHNTRIAIRLEIIGC 387
{without alignment(s)
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 478139 seqs, 63318000 residues
Total number of hits satisfying chosen parameters: 110780
Minimum DB seq length: 0
Maximum DB seq length: 10
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

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2: /cgn2_6/pctodata/1/iaa/5B_COMB_pep: *
3: /cgn2_6/pctodata/1/iaa/6A_COMB_pep: *
4: /cgn2_6/pctodata/1/iaa/6B_COMB_pep: *
5: /cgn2_6/pctodata/1/iaa/PCTUS_COMB_pep: *
6: /cgn2_6/pctodata/1/iaa/backfile1.pep: *

Pred. No. 18 the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	2.0	9	1	US-08-79-481-115 Sequence 115, APP
2	42	2.0	10	6	517197-8 Sequence No. 517197
3	39	1.8	8	3	US-08-981-322-88 Sequence 88, APP
4	39	1.8	8	4	US-09-908-322-88 Sequence 88, APP
5	37	1.8	10	1	US-09-79-481-31 Sequence 11, APP
6	36	1.7	7	2	US-08-162-402B-23 Sequence 23, APP
7	34	1.6	8	3	US-08-881-988A-29 Sequence 29, APP
8	34	1.6	8	3	US-08-54-712B-29 Sequence 29, APP
9	34	1.6	8	4	US-08-947-925A-29 Sequence 29, APP
10	34	1.6	9	2	US-08-64-60-69 Sequence 69, APP
11	34	1.6	9	3	US-08-73-252B-69 Sequence 69, APP
12	34	1.6	9	3	US-09-244-238A-69 Sequence 69, APP
13	34	1.6	9	3	US-09-316-70-69 Sequence 69, APP
14	34	1.6	9	4	US-09-449-70-69 Sequence 69, APP
15	34	1.6	9	4	US-09-832-230A-69 Sequence 69, APP
16	34	1.6	9	4	US-09-558-836C-38 Sequence 38, APP
17	34	1.6	10	2	US-08-64-60-63 Sequence 121, APP
18	34	1.6	10	2	US-08-556-597-121 Sequence 63, APP
19	34	1.6	10	3	US-08-973-225-63 Sequence 63, APP
20	34	1.6	10	3	US-09-44-238A-63 Sequence 63, APP
21	34	1.6	10	3	US-09-516-704-63 Sequence 63, APP
22	34	1.6	10	4	US-09-549-090-63 Sequence 63, APP
23	34	1.6	10	4	US-09-312-230-63 Sequence 63, APP
24	34	1.6	10	4	US-09-428-032B-46 Sequence 46, APP
25	34	1.6	10	4	US-09-663-222C-34 Sequence 34, APP
26	33	1.6	7	2	US-08-422-402B-22 Sequence 22, APP
27	33	1.6	9	2	US-08-390-268-10 Sequence 10, APP

28	33	1.6	10	2	US-08-764-640-122	Sequence 122, Appl
29	33	1.6	10	2	US-08-335-832-8	Sequence 8, Appl
30	33	1.6	10	3	US-09-141-172-2	Sequence 2, Appl
31	33	1.6	10	3	US-08-973-225-122	Sequence 122, Appl
32	33	1.6	10	3	US-09-244-298A-122	Sequence 122, Appl
33	33	1.6	10	3	US-09-516-704-122	Sequence 122, Appl
34	33	1.6	10	4	US-09-549-090-122	Sequence 122, Appl
35	33	1.6	10	4	US-09-832-230A-122	Sequence 122, Appl
36	33	1.6	10	4	US-09-535-852-122	Sequence 109B, Appl
37	33	1.6	10	4	US-09-535-852-1370	Sequence 1370, Appl
38	32	1.5	7	4	US-09-559-846-1	Sequence 1, Appl
39	32	1.5	6	5	525663-5	Patent No. 5256643
40	32	1.5	9	1	US-07-646-531D-4	Sequence 4, Appl
41	32	1.5	9	1	US-07-646-531D-19	Sequence 19, Appl
42	32	1.5	9	2	US-08-488-273-4	Sequence 4, Appl
43	32	1.5	9	3	US-08-142-590B-10	Sequence 10, Appl
44	32	1.5	9	3	US-09-139-802-113	Sequence 113, Appl
45	32	1.5	9	3	US-09-197-770B-10	Sequence 10, Appl

QY 32 CINGGLC 38 ; MOLECULE TYPE: peptide
 Db 3 CINGGQC 9 ; US-08-981-392-88
 RESULT 2
 5177197-8 ; Query Match 1.8%; Score 39; DB 3; Length 8;
 ; Patent No. 5177197 Best Local Similarity 85.7%; Pred. No. 3.8e+05;
 ; APPLICANT: KANZAKI, TETSUTO; OLOFSSON, ANDERS; MOREN, ANITA; 0; Mismatches 1; Indels 0;
 ; WERNSTEDT, CHRISTER; HELLMAN, ULF; MITAZONO, KOHEI; CLAESSEN-WELSH, 0; Gaps 0;
 ; LENA; HELLDIN, CARL-HENRIK
 ; TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING
 ; HUMAN TRANSFORMING GROWTH FACTOR-BETA1-BINDING PROTEIN
 ; NUMBER OF SEQUNENCES: 53
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/487,343
 ; FILING DATE: 27-FEB-1990
 ; SEQ ID NO:8:
 ; LENGTH: 10
 ; 5177197-8

Query Match 2.0%; Score 42; DB 6; Length 10;
 Best Local Similarity 66.7%; Pred. No. 7.9e+02; 1; Mismatches 2; Indels 0; Gaps 0;
 Matches 6; Conservative 1; Gaps 0;
 QY 53 YTCCTLKGY 61 ; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF VERTEBRATE DELTA GENE AND METHODS BASED THEREON
 Db 1 YTCCTCAGY 9 ; NUMBER OF SEQUNENCES: 94
 ; CURRENT APPLICATION DATA:
 ; APPLICANT: Ish-Horowicz, David
 ; APPLICANT: Enrique, Domingos Manuel Pinto
 ; APPLICANT: Lewis, Julian Hart
 ; APPLICANT: Artavanis-Tsakonas, Spyridon
 ; APPLICANT: Gray, Grace
 ; APPLICANT: Gray, Grace
 ; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF VERTEBRATE DELTA GENE AND METHODS BASED THEREON
 ; NUMBER OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON
 ; NUMBER OF SEQUENCES: 94
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds LLP
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10036/2711
 ; COMPUTER READABLE FORM:
 ; COMPUTER TYPE: Diskette
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FASTSEQ Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/981,392
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/981,392
 ; FILING DATE: 22-DEC-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Misrock, S Leslie
 ; NAME: Leslie
 ; REGISTRATION NUMBER: 18,872
 ; REFERENCE/DOCKET NUMBER: 7226-123
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-790-9090
 ; TELEFAX: 212-869-8864
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 88:
 ; SEQUENCE CHARACTERISTICS:
 ; MOLECULE TYPE: peptide
 ; LENGTH: 8 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: <Unknown>
 ; TOPOLOGY: unknown
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 88:
 ; US-09-908-322-88

Query Match 1.8%; Score 39; DB 4; Length 8;
 Best Local Similarity 85.7%; Pred. No. 3.8e+05;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 30 NPCHNGG 36 ; MOLECULE TYPE: peptide
 Db 1 NPCKNGG 7 ; US-09-908-322-88
 RESULT 4
 US-09-908-322-88 ; Query Match 1.8%; Score 39; DB 4; Length 8;
 ; Sequence 88, Application US/09908322
 ; Patent No. 6733956
 ; GENERAL INFORMATION:
 ; APPLICANT: Ish-Horowicz, David
 ; APPLICANT: Enrique, Domingos Manuel Pinto
 ; APPLICANT: Lewis, Julian Hart
 ; APPLICANT: Artavanis-Tsakonas, Spyridon
 ; APPLICANT: Gray, Grace
 ; APPLICANT: Gray, Grace
 ; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF VERTEBRATE DELTA GENE AND METHODS BASED THEREON
 ; NUMBER OF SEQUNENCES: 94
 ; CURRENT APPLICATION DATA:
 ; APPLICANT: Pennie & Edmonds LLP
 ; ADDRESS: 1155 Avenue of the Americas
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10036/2711
 ; COMPUTER READABLE FORM:
 ; COMPUTER TYPE: Diskette
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FASTSEQ Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/981,392
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/981,392
 ; FILING DATE: 22-DEC-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Misrock, S Leslie
 ; NAME: Leslie
 ; REGISTRATION NUMBER: 18,872
 ; REFERENCE/DOCKET NUMBER: 7226-123
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-790-9090
 ; TELEFAX: 212-869-8864
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 88:
 ; SEQUENCE CHARACTERISTICS:
 ; MOLECULE TYPE: peptide
 ; LENGTH: 8 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: <Unknown>
 ; TOPOLOGY: unknown
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 88:
 ; US-09-908-322-88

Query Match 1.8%; Score 39; DB 4; Length 8;
 Best Local Similarity 85.7%; Pred. No. 3.8e+05;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 30 NPCHNGG 36 ; MOLECULE TYPE: peptide
 Db 1 NPCKNGG 7 ; US-08-179-481-31

RESULT 5
 US-08-179-481-31

NAME: Antler, Adriane M.
 REGISTRATION NUMBER: 32,605
 REFERENCE/DOCKET NUMBER: 7326-038
 TELECOMMUNICATION INFORMATION:
 CLASSIFICATION: 514
 FILING DATE: 22-DEC-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Antler, Adriane M.
 ; REGISTRATION NUMBER: 32,605
 ; REFERENCE/DOCKET NUMBER: 7326-038
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-790-9090
 ; TELEFAX: 212-869-8864
 ; INFORMATION FOR SEQ ID NO: 88:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 8 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: <Unknown>
 ; TOPOLOGY: unknown
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 88:
 ; US-09-908-322-88

Sequence 31, Application US/08179481
 Patent No. 562816
 GENERAL INFORMATION:
 APPLICANT: CARRAWAY, KERMIT L.
 APPLICANT: CARRAWAY, CORALIE A.
 TITLE OF INVENTION: ONCOGENE PRODUCT LIGAND
 NUMBER OF SEQUENCES: 125
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
 STREET: 1100 NEW YORK AVENUE, N.W.
 CITY: WASHINGTON
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20005-3918
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/179,481
 FILING DATE: 28-DEC-1993
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/922,521
 FILING DATE: 30-JUL-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: KOKULIS, PAUL N.
 REGISTRATION NUMBER: 16,773
 REFERENCE/DOCKET NUMBER: 200702/UM92-08CIP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 861-3000
 TELEFAX: (202) 822-0944
 TELEX: 6714627 CUSH
 INFORMATION FOR SEQ ID NO: 31:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-179-481-31
 Query Match 1.8%; Score 37; DB 1; Length 10;
 Best Local Similarity 85.7%; Pred. No. 2.3e+03;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY |||||
 Db 1 WAPBLAR 7
 BY 30 NPCHNG 36
 3 NPCLNG 9
 RESULT 6
 Sequence 23, Application US/08162402B
 Patent No. 5972337
 GENERAL INFORMATION:
 APPLICANT: CERTANI, ROBERTO L.
 APPLICANT: PETERSON, JERRY A.
 APPLICANT: LAROCCA, DAVID J.
 TITLE OF INVENTION: 46 KDALTON HUMAN MILK FAT
 TITLE OF INVENTION: GLOBULE (HMFG) ANTIGEN, FRAGMENTS & FUSION PROTEIN
 NUMBER OF SEQUENCES: 29
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Prety, Schroeder & Poplawski
 STREET: 444 South Flower St., 19th Floor
 CITY: Los Angeles
 STATE: CA
 COUNTRY: USA
 ZIP: 90071
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 RESULT 8
 US-08-154-712B-29
 ; Sequence 29, Application US/08154712B
 ; Patent No. 6337209
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/162,402B
 FILING DATE: 03-DEC-1993
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Amel, Viviana
 REGISTRATION NUMBER: 30,930
 REFERENCE/DOCKET NUMBER: P66 38215
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 213-622-7700
 TELEFAX: 213-489-4210
 INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 7 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: Peptide
 US-08-162-402B-23
 Query Match 1.7%; Score 36; DB 2; Length 7;
 Best Local Similarity 85.7%; Pred. No. 3.8e+05;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 101 WVPILLAR 107
 Db 1 WAPBLAR 7
 BY 30 NPCHNG 36
 3 NPCLNG 9
 RESULT 7
 US-08-481-968A-29
 ; Sequence 29, Application US/08481968A
 ; Patent No. 6300490
 ; GENERAL INFORMATION:
 ; APPLICANT: Huber, Brian
 ; APPLICANT: Richards, Cynthia
 ; TITLE OF INVENTION: Molecular Constructs Comprising a Carcinoembryonic Antigen (CEA) Transcriptional Regulatory Region
 ; FILE REFERENCE: PBL087US4
 ; CURRENT APPLICATION NUMBER: US/08/481,968A
 ; CURRENT FILING DATE: 1998-06-07
 ; NUMBER OF SEQ ID NOS: 36
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 29
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Consensus sequence
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Consensus Sequence P6 from transcriptional dictionary of Locker a
 ; OTHER INFORMATION: nd Buzard (1990);
 US-08-481-968A-29
 Query Match 1.6%; Score 34; DB 3; Length 8;
 Best Local Similarity 71.4%; Pred. No. 3.8e+05;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 211 SCKFACT 217
 Db 1 TCKFACT 7
 RESULT 8
 US-08-154-712B-29
 ; Sequence 29, Application US/08154712B
 ; Patent No. 6337209

GENERAL INFORMATION:
 APPLICANT: Huber, Brian
 APPLICANT: Richards, Cynthia
 TITLE OF INVENTION: Molecular Constructs Containing a Carcinoembryonic Antigen Receptor
 FILE REFERENCE: PB1037U3
 CURRENT APPLICATION NUMBER: US/08/154,712B
 CURRENT FILING DATE: 1993-11-19
 NUMBER OF SEQ ID NOS: 36
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 29
 LENGTH: 8
 TYPE: PRT
 ORGANISM: Consensus sequence
 FEATURE:
 NAME/KEY: misc feature
 OTHER INFORMATION: Consensus sequence F6 from transcriptional dictionary of Locker a
 US-08-154-712B-29

Query Match 1.6%; Score 34; DB 3; Length 8;
 Best Local Similarity 71.4%; Pred. No. 3.8e+05; Indels 0; Gaps 0;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 211 SCHFACT 217
 DB 1 TCTFACT 7

RESULT 9
 US-09-947-925A-29
 Sequence 29, Application US/09947925A
 Patent No. 6699390
 GENERAL INFORMATION:
 APPLICANT: Huber, Brian
 APPLICANT: Richards, Cynthia
 APPLICANT: Richards, Cynthia
 TITLE OF INVENTION: Molecular Constructs Containing a Carcinoembryonic
 TITLE OF INVENTION: Antigen Regulatory
 TITLE OF INVENTION: Sequence
 FILE REFERENCE: PB1087U3
 CURRENT APPLICATION NUMBER: US/09/947,925A
 CURRENT FILING DATE: 2001-09-06
 PRIOR APPLICATION NUMBER: US/08/154,712
 PRIOR FILING DATE: 1993-11-19
 NUMBER OF SEQ ID NOS: 36
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 29
 LENGTH: 8
 TYPE: PRT
 ORGANISM: Consensus sequence
 FEATURE:
 NAME/KEY: misc feature
 OTHER INFORMATION: Consensus sequence F6 from transcriptional dictionary
 OTHER INFORMATION: Consensus sequence F6 from transcriptional dictionary
 OTHER INFORMATION: nd Buzzard (1990).
 US-09-947-925A-29

Query Match 1.6%; Score 34; DB 4; Length 8;
 Best Local Similarity 71.4%; Pred. No. 3.8e+05; Indels 0; Gaps 0;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 211 SCHFACT 217
 DB 1 TCTFACT 7

RESULT 10
 US-08-947-925A-29
 Sequence 29, Application US/09947925A
 Patent No. 6699390
 GENERAL INFORMATION:
 APPLICANT: Dower, William J.
 APPLICANT: Barrett, Ronald W.
 APPLICANT: Chirila, Steven E.
 APPLICANT: Druffin, David J.
 APPLICANT: Gates, Christian
 APPLICANT: Haselden, Sheril S.
 APPLICANT: Mattheakis, Larry C.
 APPLICANT: Schatz, Peter J.
 APPLICANT: Wigstrom, Christopher R.
 APPLICANT: Wrighton, Nicholas C.
 Sequence 69, Application US/08764640
 Patent No. 5669451
 Patent No. 5669451 5831683
 GENERAL INFORMATION:
 APPLICANT: Dower, William J.

RESULT 10
 US-08-764-640-69
 Sequence 69, Application US/08764640
 Patent No. 5669451
 Patent No. 5669451 5831683
 GENERAL INFORMATION:
 APPLICANT: Dower, William J.

RESULT 11
 US-08-913-225-69
 Sequence 69, Application US/08973225A
 Patent No. 6083913
 GENERAL INFORMATION:
 APPLICANT: Dower, William J.
 APPLICANT: Barrett, Ronald W.
 APPLICANT: Chirila, Steven E.
 APPLICANT: Druffin, David J.
 APPLICANT: Gates, Christian
 APPLICANT: Haselden, Sheril S.
 APPLICANT: Mattheakis, Larry C.
 APPLICANT: Schatz, Peter J.
 APPLICANT: Wigstrom, Christopher R.
 APPLICANT: Wrighton, Nicholas C.
 TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
 NUMBER OF SEQUENCES: 232
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Glaxo Wellcome

STREET: Five Moore Drive, P.O. Box 13398
 CITY: Research Triangle Park
 STATE: NC
 COUNTRY: USA
 ZIP: 27709.

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/973,225A

FILED DATE: 04-Dec-1997

ATTORNEY/AGENT INFORMATION:
 NAME: Hrubiec, Robert T.

REGISTRATION NUMBER: 36,392

REFERENCE/DOCKET NUMBER: PK3281

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 919-248-1000

INFORMATION FOR SEQ ID NO: 69:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: Peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 69:

INFORMATION FOR SEQ ID NO: 69:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: Peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 69:

Query Match 1.6%; Score 34; DB 3; Length 9;
 Best Local Similarity 46.7%; Pred. No. 3 8e+05; 1; Indels
 Matches 7; Conservative 1; Mismatches 1; Gaps 1;
 Qy 216 CTRPFLIGCENG 230
 Db 1 CTLEP----MNGC 9

RESULT 12
 US-09-244-298A-59

; Sequence 69, Application US/09244298A

; GENERAL INFORMATION:

APPLICANT: Dower, William J.

APPLICANT: Barrett, Ronald W.

APPLICANT: Cwirla, Steven E.

APPLICANT: Gates, Christian

APPLICANT: Schatz, Peter J.

APPLICANT: Balasubramanian, Palaniappan

APPLICANT: Wagstrom, Christopher R.

APPLICANT: Hendren, Richard W.

APPLICANT: Deprince, Randolph B.

APPLICANT: Podduturi, Surekha

APPLICANT: Yin, Qun

TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A

NUMBER OF SEQUENCES: 244
 TITLE OF INVENTION: RECEPTOR

NUMBER OF SEQUENCES: 244
 NUMBER OF SEQUENCES: 244

CORRESPONDENCE ADDRESS:
 ADDRESS: Glaxo Wellcome

CITY: Research Triangle Park

STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/516,704

FILED DATE: 01-Mar-2000

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:
 NAME: Hrubiec, Robert T.

REGISTRATION NUMBER: 36,392

REFERENCE/DOCKET NUMBER: PK3281

INFORMATION FOR SEQ ID NO: 69:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>

MOLECULE TYPE: Peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 69:

INFORMATION FOR SEQ ID NO: 69:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>

MOLECULE TYPE: Peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 69:

INFORMATION FOR SEQ ID NO: 69:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>

MOLECULE TYPE: Peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 69:

Query Match 1.6%; Score 34; DB 3; Length 9;

Best Local Similarity 46.7%; Pred. No. 3.8e+05; 1; Mismatches 1; Indels 6; Gaps 1;

Matches 7; Conservative

Qy

216 CTLRFLGICELNGC 230

Db

1 CTLER-----MNGC 9

RESULT 14

US-09-549-090-69

Sequence 69, Application US/09549090

Patent No. 6,455,430

GENERAL INFORMATION:

APPLICANT: Dower, William J. et al

TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A

NUMBER OF SEQUENCES: 244

CORRESPONDENCE ADDRESS:

ADDRESSEE: Glaxo Wellcome

STREET: Five Moore Drive, P.O. Box 13398

CITY: Research Triangle Park

STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENT-IN RELEASE #1.0, VERSION #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/832,230A

FILING DATE: 10-APR-2001

CLASSIFICATION: <UNKNOWN>

ATTORNEY/AGENT INFORMATION:

NAME: Hrubiec, Robert T.

REGISTRATION NUMBER: 36,392

REFERENCE/DOCKET NUMBER: PR3281

TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-248-1000

INFORMATION FOR SEQ ID NO: 69:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

STRANDNESS: <UNKNOWN>

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 69:

US-09-832-230A-69

Query Match 1.6%; Score 34; DB 4; Length 9;

Best Local Similarity 46.7%; Pred. No. 3.8e+05; 1; Mismatches 1; Indels 6; Gaps 1;

Matches 7; Conservative

Qy

216 CTLRFLGICELNGC 230

Db

1 CTLER-----MNGC 9

RESULT 15

US-09-549-090-69

Query Match 1.6%; Score 34; DB 4; Length 9;

Best Local Similarity 46.7%; Pred. No. 3.8e+05; 1; Mismatches 1; Indels 6; Gaps 1;

Matches 7; Conservative

Qy

216 CTLRFLGICELNGC 230

Db

1 CTLER-----MNGC 9